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1600

## RAW SEQUENCE LISTING

DATE: 09/26/2003

PATENT APPLICATION: US/09/706,128A

TIME: 15:58:57

Input Set : A:\VPI98-04 CON.APP

Output Set: N:\CRF4\09262003\I706128A.raw

3 <110> APPLICANT: XIE, XIAOLING  
4 GU, YONG  
5 MARKLAND, WILLIAM  
6 SU, MICHAEL S.  
7 CARON, PAUL R.  
8 FOX, EDWARD  
9 WILSON, KEITH P.  
11 <120> TITLE OF INVENTION: CRYSTALLIZABLE JNK COMPLEXES  
13 <130> FILE REFERENCE: VPI/98-04 CON  
15 <140> CURRENT APPLICATION NUMBER: 09/706,128A  
16 <141> CURRENT FILING DATE: 2000-11-03  
18 <150> PRIOR APPLICATION NUMBER: PCT/US99/09824  
19 <151> PRIOR FILING DATE: 1999-05-04  
21 <150> PRIOR APPLICATION NUMBER: 60/084,056  
22 <151> PRIOR FILING DATE: 1998-05-04  
24 <160> NUMBER OF SEQ ID NOS: 9  
26 <170> SOFTWARE: PatentIn Ver. 2.1  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 422  
30 <212> TYPE: PRT  
31 <213> ORGANISM: Homo sapiens  
33 <220> FEATURE:  
34 <223> OTHER INFORMATION: JNK3  
36 <400> SEQUENCE: 1  
37 Met Ser Leu His Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu Asp Val  
38 1 5 10 15  
40 Lys Ile Ala Phe Cys Gln Gly Phe Asp Lys Gln Val Asp Val Ser Tyr  
41 20 25 30  
43 Ile Ala Lys His Tyr Asn Met Ser Lys Ser Lys Val Asp Asn Gln Phe  
44 35 40 45  
46 Tyr Ser Val Glu Val Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr  
47 50 55 60  
49 Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val Cys Ala  
50 65 70 75 80  
52 Ala Tyr Asp Ala Val Leu Asp Arg Asn Val Ala Ile Lys Lys Leu Ser  
53 85 90 95  
55 Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr Arg Glu Leu  
56 100 105 110  
58 Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Ser Leu Leu Asn  
59 115 120 125  
61 Val Phe Thr Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu  
62 130 135 140  
64 Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile Gln Met Glu

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65 145          150          155          160
67 Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly
68          165          170          175
70 Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp Leu Lys Pro
71          180          185          190
73 Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe
74          195          200          205
76 Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr Pro Tyr Val
77          210          215          220
79 Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly Met Gly Tyr
80 225          230          235          240
82 Lys Glu Asn Val Asp Ile Trp Ser Val Gly Cys Ile Met Gly Glu Met
83          245          250          255
85 Val Arg His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp
86          260          265          270
88 Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe Met Lys
89          275          280          285
91 Lys Leu Gln Pro Thr Val Arg Asn Tyr Val Glu Asn Arg Pro Lys Tyr
92          290          295          300
94 Ala Gly Leu Thr Phe Pro Lys Leu Phe Pro Asp Ser Leu Phe Pro Ala
95 305          310          315          320
97 Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu
98          325          330          335
100 Ser Lys Met Leu Val Ile Asp Pro Ala Lys Arg Ile Ser Val Asp Asp
101          340          345          350
103 Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro Ala Glu Val
104          355          360          365
106 Glu Ala Pro Pro Pro Gln Ile Tyr Asp Lys Gln Leu Asp Glu Arg Glu
107          370          375          380
109 His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val Met Asn
110 385          390          395          400
112 Ser Glu Glu Lys Thr Lys Asn Gly Val Val Lys Gly Gln Pro Ser Pro
113          405          410          415
115 Ser Ala Gln Val Gln Gln
116          420
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120 <211> LENGTH: 39
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
124 <220> FEATURE:
125 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
127 <400> SEQUENCE: 2
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131 <210> SEQ ID NO: 3
132 <211> LENGTH: 37
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <223> OTHER INFORMATION: Description of Artificial Sequence: primer

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144 <211> LENGTH: 8
145 <212> TYPE: PRT
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Description of Artificial Sequence: glycine-rich
150     phosphate anchor loop
152 <220> FEATURE:
153 <221> NAME/KEY: MOD_RES
154 <222> LOCATION: (2)
155 <223> OTHER INFORMATION: any amino acid
157 <220> FEATURE:
158 <221> NAME/KEY: MOD_RES
159 <222> LOCATION: (4)..(5)
160 <223> OTHER INFORMATION: any amino acid
162 <220> FEATURE:
163 <221> NAME/KEY: MOD_RES
164 <222> LOCATION: (7)..(8)
165 <223> OTHER INFORMATION: any amino acid
167 <400> SEQUENCE: 4
W--> 168 Gly Xaa Gly Xaa Xaa Gly Xaa Xaa
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173 <211> LENGTH: 8
174 <212> TYPE: PRT
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Artificial Sequence: glycine-rich
179     peptide
181 <400> SEQUENCE: 5
182 Gly Ser Gly Ala Gln Gly Ile Val
183     1             5
186 <210> SEQ ID NO: 6
187 <211> LENGTH: 21
188 <212> TYPE: PRT
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: Description of Artificial Sequence: EGF receptor
193     peptide
195 <400> SEQUENCE: 6
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197     1             5             10             15
199 Gln Ala Leu Leu Arg
200             20
203 <210> SEQ ID NO: 7
204 <211> LENGTH: 340
205 <212> TYPE: PRT

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206 <213> ORGANISM: Homo sapiens  
 208 <220> FEATURE:  
 209 <223> OTHER INFORMATION: p38  
 211 <400> SEQUENCE: 7  
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 213 1 5 10 15  
 215 Tyr Gln Asn Leu Ser Pro Val Gly Ser Gly Ala Tyr Gly Ser Val Cys  
 216 20 25 30  
 218 Ala Ala Phe Asp Thr Lys Thr Gly Leu Arg Val Ala Val Lys Lys Leu  
 219 35 40 45  
 221 Ser Arg Pro Phe Gln Ser Ile Ile His Ala Lys Arg Thr Tyr Arg Glu  
 222 50 55 60  
 224 Leu Arg Leu Leu Lys His Met Lys His Glu Asn Val Ile Gly Leu Leu  
 225 65 70 75 80  
 227 Asp Val Phe Thr Pro Ala Arg Ser Leu Glu Glu Phe Asn Asp Val Tyr  
 228 85 90 95  
 230 Leu Val Thr His Leu Met Gly Ala Asp Leu Asn Asn Ile Val Lys Cys  
 231 100 105 110  
 233 Gln Lys Leu Thr Asp Asp His Val Gln Phe Leu Ile Tyr Gln Ile Leu  
 234 115 120 125  
 236 Arg Gly Leu Lys Tyr Ile His Ser Ala Asp Ile Ile His Arg Asp Leu  
 237 130 135 140  
 239 Lys Pro Ser Asn Leu Ala Val Asn Glu Asp Cys Glu Leu Lys Ile Leu  
 240 145 150 155 160  
 242 Asp Phe Gly Leu Ala Arg His Thr Asp Asp Glu Met Thr Gly Tyr Val  
 243 165 170 175  
 245 Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Trp Met His  
 246 180 185 190  
 248 Tyr Asn Gln Thr Val Asp Ile Trp Ser Val Gly Cys Ile Met Ala Glu  
 249 195 200 205  
 251 Leu Leu Thr Gly Arg Thr Leu Phe Pro Gly Thr Asp His Ile Asp Gln  
 252 210 215 220  
 254 Leu Lys Leu Ile Leu Arg Leu Val Gly Thr Pro Gly Ala Glu Leu Leu  
 255 225 230 235 240  
 257 Lys Lys Ile Ser Ser Glu Ser Ala Arg Asn Tyr Ile Gln Ser Leu Thr  
 258 245 250 255  
 260 Gln Met Pro Lys Met Asn Phe Ala Asn Val Phe Ile Gly Ala Asn Pro  
 261 260 265 270  
 263 Leu Ala Val Asp Leu Leu Glu Lys Met Leu Val Leu Asp Ser Asp Lys  
 264 275 280 285  
 266 Arg Ile Thr Ala Ala Gln Ala Leu Ala His Ala Tyr Phe Ala Gln Tyr  
 267 290 295 300  
 269 His Asp Pro Asp Asp Glu Pro Val Ala Asp Pro Tyr Asp Gln Ser Phe  
 270 305 310 315 320  
 272 Glu Ser Arg Asp Leu Leu Ile Asp Glu Trp Lys Ser Leu Thr Tyr Asp  
 273 325 330 335  
 275 Glu Val Ile Ser  
 276 340  
 279 <210> SEQ ID NO: 8

## RAW SEQUENCE LISTING

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280 <211> LENGTH: 342
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens
284 <220> FEATURE:
285 <223> OTHER INFORMATION: ERK2
287 <400> SEQUENCE: 8
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289   1           5           10           15
291 Tyr Thr Asn Leu Ser Tyr Ile Gly Glu Gly Ala Tyr Gly Met Val Cys
292           20           25           30
294 Ser Ala Tyr Asp Asn Val Asn Lys Val Arg Val Ala Ile Lys Lys Ile
295           35           40           45
297 Ser Pro Phe Glu His Gln Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile
298           50           55           60
300 Lys Ile Leu Leu Arg Phe Arg His Glu Asn Ile Ile Gly Ile Asn Asp
301   65           70           75           80
303 Ile Ile Arg Ala Pro Thr Ile Glu Gln Met Lys Asp Val Tyr Ile Val
304           85           90           95
306 Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys Leu Leu Lys Thr Gln His
307           100          105          110
309 Leu Ser Asn Asp His Ile Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly
310           115          120          125
312 Leu Lys Tyr Ile His Ser Ala Asn Val Leu His Arg Asp Leu Lys Pro
313           130          135          140
315 Ser Asn Leu Leu Leu Asn Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe
316  145           150          155          160
318 Gly Leu Ala Arg Val Ala Asp Pro Asp His Asp His Thr Gly Phe Leu
319           165          170          175
321 Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu
322           180          185          190
324 Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp Ile Trp Ser Val Gly Cys
325           195          200          205
327 Ile Leu Ala Glu Met Leu Ser Asn Arg Pro Ile Phe Pro Gly Lys His
328           210          215          220
330 Tyr Leu Asp Gln Leu Asn His Ile Leu Gly Ile Leu Gly Ser Pro Ser
331  225          230          235          240
333 Gln Glu Asp Leu Asn Cys Ile Ile Asn Leu Lys Ala Arg Asn Tyr Leu
334           245          250          255
336 Leu Ser Leu Pro His Lys Asn Lys Val Pro Trp Asn Arg Leu Phe Pro
337           260          265          270
339 Asn Ala Asp Ser Lys Ala Leu Asp Leu Leu Asp Lys Met Leu Thr Phe
340           275          280          285
342 Asn Pro His Lys Arg Ile Glu Val Glu Gln Ala Leu Ala His Pro Tyr
343           290          295          300
345 Leu Glu Gln Tyr Tyr Asp Pro Ser Asp Glu Pro Ile Ala Glu Ala Pro
346  305          310          315          320
348 Phe Lys Phe Asp Met Glu Leu Asp Asp Leu Pro Lys Glu Lys Leu Lys
349           325          330          335
351 Glu Leu Ile Phe Glu Glu

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 2,4,5,7,8